

SEQUENCE LISTING

<110> Bennett, Michele
Brodbeck, Robbin
Krause, James

<120> Chimeric Neuropeptide Y Receptors

<130> N2000.001

<140> Not Yet Assigned

<141> 2000-01-28

<160> 31

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

Variable	Mean	SD	Min	Max
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Gender	Male	10.5	0	20
Marital Status	Married	15.2	0	30
Education	High School	12.5	0	25
Occupation	Manager	18.5	0	35
Income	\$45,000	\$15,000	\$20,000	\$80,000
Health Status	Good	10.5	0	20
Exercise Frequency	Weekly	12.5	0	25
Dietary Habits	Healthy	15.2	0	30
Stress Level	Low	10.5	0	20
Sleep Quality	Good	12.5	0	25
Mental Health	Stable	15.2	0	30
Life Satisfaction	High	18.5	0	35
Work-Life Balance	Good	10.5	0	20
Family Support	Strong	12.5	0	25
Community Involvement	Active	15.2	0	30
Personal Growth	High	18.5	0	35
Resilience	Strong	10.5	0	20
Emotional Stability	Good	12.5	0	25
Relationship Quality	High	15.2	0	30
Overall Well-being	Excellent	18.5	0	35

Met 1	Asn	Ser	Thr	Leu 5	Phe	Ser	Gln	Val	Glu 10	Asn	His	Ser	Val	His 15	Ser
Asn	Phe	Ser	Glu 20	Lys	Asn	Ala	Gln	Leu 25	Leu	Ala	Phe	Glu	Asn 30	Asp	Asp
Cys	His	Leu 35	Pro	Leu	Ala	Met	Ile 40	Phe	Thr	Leu	Ala	Leu 45	Ala	Tyr	Gly
Ala	Val 50	Ile	Ile	Leu	Gly	Val 55	Ser	Gly	Asn	Leu	Ala 60	Leu	Ile	Ile	Ile
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Thr	Phe	Val	Tyr 100	Thr	Leu	Met	Asp	His 105	Trp	Val	Phe	Gly	Glu 110	Ala	Met
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Gln	Val	Met	Thr 180	Asp	Glu	Pro	Phe	Gln 185	Asn	Val	Thr	Leu	Asp 190	Ala	Tyr
Lys	Asp	Lys 195	Tyr	Val	Cys	Phe	Asp 200	Gln	Phe	Pro	Ser	Asp 205	Ser	His	Arg
Leu 210	Ser	Tyr	Thr	Thr	Leu	Leu 215	Leu	Val	Leu	Gln	Tyr 220	Phe	Gly	Pro	Leu
Cys 225	Phe	Ile	Phe	Ile	Cys 230	Tyr	Phe	Lys	Ile	Tyr 235	Ile	Arg	Leu	Lys	Arg 240
Arg	Asn	Asn	Met	Met 245	Asp	Lys	Met	Arg	Asp 250	Asn	Lys	Tyr	Arg	Ser 255	Ser
Glu	Thr	Lys	Arg 260	Ile	Asn	Ile	Met	Leu 265	Leu	Ser	Ile	Val	Val 270	Ala	Phe
Ala	Val	Cys 275	Trp	Leu	Pro	Leu	Thr 280	Ile	Phe	Asn	Thr	Val 285	Phe	Asp	Trp
Asn	His 290	Gln	Ile	Ile	Ala	Thr 295	Cys	Asn	His	Asn	Leu 300	Leu	Phe	Leu	Leu

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
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 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
 325 330 335
 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
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 35 40 45
 Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
 50 55 60
 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
 65 70 75 80
 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
 85 90 95
 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
 100 105 110
 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
 115 120 125
 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
 130 135 140
 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
 145 150 155 160
 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln

165										170					175															
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Phe	Ile	Phe	Ile	Cys	Tyr	Phe	Lys	Ile	Tyr	Ile	Arg	Leu	Lys	Arg	Arg															
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Asn	Asn	Met	Met	Asp	Lys	Ile	Arg	Asp	Ser	Lys	Tyr	Arg	Ser	Ser	Glu															
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Thr	Lys	Arg	Ile	Asn	Val	Met	Leu	Leu	Ser	Ile	Val	Val	Ala	Phe	Ala															
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<400> 4
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Glu	Tyr	Tyr	Asn	Lys	Thr	Leu	Ala	Thr	Glu	Asn	Asn	Thr	Ala	Ala	Thr	
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Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu	Leu	
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His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	Arg	Asn	Asn	Met	Met	Asp	
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Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	Arg	Ser	Arg	Ser	Val	Phe	
			260					265					270			
Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro	
		275					280					285				
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Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met	
	305				310					315					320	

The following is a list of the amino acids in the protein sequence. The amino acids are listed in the order they appear in the sequence, with their corresponding three-letter codes and one-letter codes. The amino acids are: Glu, Tyr, Tyr, Asn, Lys, Thr, Leu, Ala, Thr, Glu, Asn, Asn, Thr, Ala, Ala, Thr, Arg, Asn, Ser, Asp, Phe, Pro, Val, Trp, Asp, Asp, Tyr, Lys, Ser, Ser, Val, Asp, Asp, Leu, Gln, Tyr, Phe, Leu, Ile, Gly, Leu, Tyr, Thr, Phe, Val, Ser, Leu, Leu, Gly, Phe, Met, Gly, Asn, Leu, Leu, Ile, Leu, Met, Ala, Leu, Met, Lys, Lys, Arg, Asn, Gln, Lys, Thr, Thr, Val, Asn, Phe, Leu, Ile, Gly, Asn, Leu, Ala, Phe, Ser, Asp, Ile, Leu, Val, Val, Leu, Phe, Cys, Ser, Pro, Phe, Thr, Leu, Thr, Ser, Val, Leu, Leu, Asp, Gln, Trp, Met, Phe, Gly, Lys, Val, Met, Cys, His, Ile, Met, Pro, Phe, Leu, Gln, Cys, Val, Ser, Val, Leu, Val, Ser, Thr, Leu, Ile, Leu, Ile, Ser, Ile, Ala, Ile, Val, Arg, Tyr, His, Met, Ile, Lys, His, Pro, Ile, Ser, Asn, Asn, Leu, Thr, Ala, Asn, His, Gly, Tyr, Phe, Leu, Ile, Ala, Thr, Val, Trp, Thr, Leu, Gly, Phe, Ala, Ile, Cys, Ser, Pro, Leu, Pro, Val, Phe, His, Ser, Leu, Val, Glu, Leu, Gln, Glu, Thr, Phe, Gly, Ser, Ala, Leu, Leu, Ser, Ser, Arg, Tyr, Leu, Cys, Val, Glu, Ser, Trp, Pro, Ser, Asp, Ser, Tyr, Arg, Ile, Ala, Phe, Thr, Ile, Ser, Leu, Leu, Leu, Val, Gln, Tyr, Ile, Leu, Pro, Leu, Val, Cys, Leu, Thr, Val, Ser, His, Thr, Ser, Val, Cys, Ile, Arg, Leu, Lys, Arg, Arg, Asn, Asn, Met, Met, Asp, Lys, Met, Arg, Asp, Asn, Lys, Tyr, Arg, Ser, Ser, Arg, Ser, Arg, Ser, Val, Phe, Tyr, Arg, Leu, Thr, Ile, Leu, Ile, Leu, Val, Phe, Ala, Val, Ser, Trp, Met, Pro, Leu, His, Leu, Phe, His, Val, Val, Thr, Asp, Phe, Asn, Asp, Asn, Leu, Ile, Ser, Asn, Arg, His, Phe, Lys, Leu, Val, Tyr, Cys, Ile, Cys, His, Leu, Leu, Gly, Met

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 Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
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 Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
 195 200 205
 Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
 210 215 220
 Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
 225 230 235 240
 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu
 245 250 255
 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser
 260 265 270
 Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser
 275 280 285
 Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala
 290 295 300
 Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg
 305 310 315 320
 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser
 325 330 335
 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu
 340 345 350
 Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg
 355 360 365
 Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
 370 375 380
 Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val
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 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
 405 410 415
 Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
 420 425 430
 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe
 435 440 445
 Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr
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35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys

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Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser
210						215					220				
Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser
225					230					235					240
His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	Arg	Asn	Asn	Met	Met	Asp
				245					250					255	
Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	Arg	Ser	Arg	Ser	Val	Phe
			260					265					270		
Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro
			275				280					285			
Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser
	290					295					300				
Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met
305					310					315					320
Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn	Gly
				325					330					335	
Ile	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser
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Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	Ser	Thr	Met	His	Thr	Asp
			355				360					365			
Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	Pro	Val	Ala	Phe	Lys	Lys
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 His His His His His His
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TAG

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<210> 13

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<213> Homo sapiens

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Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
 225 230 235 240
 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu
 245 250 255
 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser
 260 265 270
 Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser
 275 280 285
 Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala
 290 295 300
 Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg
 305 310 315 320
 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser
 325 330 335
 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu
 340 345 350
 Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg
 355 360 365
 Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
 370 375 380
 Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val
 385 390 395 400
 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
 405 410 415
 Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
 420 425 430
 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Val Ser
 435 440 445
 Leu Ile His Cys Leu His Met
 450 455

<210> 14
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 14
 ttttggttgc tgacaaatgt c

<210> 15

<211> 26
<212> DNA
<213> Homo sapiens

<400> 15
ccttggtataa cagtgagaat tattac

26

<210> 16
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5
PRIMER

<400> 16
tacgcctaaa aaggagaaac aacatgatgg acaagatgag agacaataag tacaggtcca 60
gta 63

<210> 17
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5
PRIMER

<400> 17
gatctactgg acctgtactt attgtctctc atcttgtcca tcatgttggt tctccttttt 60
aggcgtatgc a 71

<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MUTAGENIC R1
PRIMER

<400> 18
gaacaaaaga attcagagag acttgcagtt c

31

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MUTAGENIC R1
PRIMER

<400> 19
cagcttgaat tccattatta agaaaccc

28

<210> 20
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 20
Met Asp Leu Glu Leu Gln Asp Phe Tyr Asn Lys Thr Leu Ala Thr Glu
1 5 10 15
Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30
Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45
Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60
Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile
65 70 75 80
Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95
Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110
Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140
His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160
Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175
Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu
180 185 190
Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
195 200 205
Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu
210 215 220
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg

225		230		235		240
Arg Asn Asn Met	Met Asp Lys Met	Arg Asp Asn Lys Tyr Arg	Ser Ser			
	245	250	255			
Arg Ser Arg Ser	Val Phe Tyr Arg	Leu Thr Ile Leu Ile	Leu Val Phe			
	260	265	270			
Ala Val Ser Trp	Met Pro Leu His	Leu Phe His Val	Val Thr Asp Phe			
	275	280	285			
Asn Asp Asn Leu	Ile Ser Asn Arg	His Phe Lys Leu	Val Tyr Cys Ile			
	290	295	300			
Cys His Leu Leu	Gly Met Met Ser	Cys Cys Leu Asn	Pro Ile Leu Tyr			
305	310	315	320			
Gly Phe Leu Asn	Asn Gly Ile Lys	Ala Asp Leu Ile	Ser Leu Ile Gln			
	325	330	335			
Cys Leu His Met	Ser					
	340					

<210> 21
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 21															
Met	Asp	Leu	Glu	Leu	Gln	Asp	Phe	Tyr	Asn	Lys	Thr	Leu	Ala	Thr	Glu
1				5					10					15	
Asn	Asn	Thr	Ala	Ala	Thr	Arg	Asn	Ser	Asp	Phe	Pro	Val	Trp	Asp	Asp
			20					25					30		
Tyr	Lys	Ser	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr
		35					40					45			
Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met
	50					55					60				
Ala	Leu	Met	Arg	Lys	Arg	Asn	Gln	Lys	Thr	Met	Val	Asn	Phe	Leu	Ile
65					70					75				80	
Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro
				85					90					95	
Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Val
		100						105					110		
Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser
		115					120					125			

Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly
 325 330 335

Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met
 340 345 350

<210> 7
 <211> 1500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 7
 atgtcttttt attccaagca ggactataat atggatttag agctcgacga gtattataac 60
 aagacacttg ccacagagaa taatactgct gccactcgga attctgattt cccagtctgg 120
 gatgactata aaagcagtgat agatgactta cagtattttc tgattgggct ctatacattt 180
 gtaagtcttc ttggctttat ggggaatcta cttattttta tggctctcat gaaaaagcgt 240
 aatcagaaga ctacggtaaa cttcctcata ggcaatctgg ctttttctga tatcttggtt 300
 gtgctgtttt gctcaccttt cacactgaag tctgtcttgc tggatcagtg gatgtttggc 360
 aaagtcattg gccatattat gccttttctt caatgtgtgt cagttttggt ttcaacttta 420
 attttaatat caattgccat tgtcaggat catatgataa aacatcccat atctaataat 480
 ttaacagcaa accatggcta ctttctgata gctactgtct ggacactagg ttttgccatc 540
 tgttctcccc ttccagtgtt tcacagtctt gtggaacttc aagaaacatt tggttcagca 600
 ttgctgagca gcagggtatt atgtgttgag tcatggccat ctgattcata cagaattgcc 660
 tttactatct ctttattgct agttcagtat attctgccct tagtttgtct tactgtaagt 720
 catacaagtg tctgcagaag tataagctgt ggattgtcca acaaagaaaa cagacttgaa 780
 gaaaatgaga tgatcaactt aactcttcat ccatccaaaa agagtgggcc tcagggtgaa 840
 ctctctggca gccataaatg gagttattca ttcatacaaaa aacacagaag aagatatagc 900
 aagaagacag catgtgtgtt acctgtctca gaaagacctt ctcaagagaa ccaactccaga 960
 atacttccag aaaacttttg ctctgtaaga agtcagctct cttcatccag taagttcata 1020
 ccagggtcc cacttgctt tgagataaaa cctgaagaaa attcagatgt tcatgaattg 1080
 agagtaaaac gttctgttac aagaataaaa aagagatctc gaagtgtttt ctacagactg 1140
 accatactga tattagtatt tgctgttagt tggatgccac tacacctttt ccatgtggta 1200
 actgatttta atgacaatct tatttcaaag aggcatttca agttggtgta ttgcatttgt 1260
 catttgttgg gcatgatgtc ctgttgtctt aatccaattc tatatgggtt tcttaataat 1320
 ggaattcaga gagacttgca gttcttcttc aacttttgtg atttcgggtc tcgggatgat 1380
 gattatgaaa caatagccat gtccacgatg cacacagatg tttccaaaac ttctttgaag 1440
 caagcaagcc cagtcgcatt taaaaaatc aacaacaatg atgataatga aaaaatctga 1500

<210> 8
 <211> 1201
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 8
 ttttgggtgc tgacaaatgt ctttttattc caagcaggac tataatatgg atttagagct 60
 cgacgagtat tataacaaga cacttgccac agagaataat actgctgcca ctcggaattc 120
 tgatttccca gtctgggatg actataaaaag cagtgtagat gacttacagt attttctgat 180
 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaattgc 240

Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	130	135	140
His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	145	150	155
Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	165	170	175
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Thr	Phe	Asp	Ser	Ala	Leu	Leu	180	185	190
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	195	200	205
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	210	215	220
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	225	230	235
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	245	250	255
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	260	265	270
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	275	280	285
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	290	295	300
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	305	310	315
Gly	Phe	Leu	Asn	Asn	Gly	Ile	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	325	330	335
Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	340	345	350
Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	355	360	365
Pro	Val	Ala	Phe	Lys	Lys	Ile	Asn	Asn	Asp	Asp	Asn	Glu	Lys	Ile		370	375	380

<210> 22

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

Parameter	Value	Unit
α	0.001	
β	0.001	
γ	0.001	
δ	0.001	
ϵ	0.001	
ζ	0.001	
η	0.001	
θ	0.001	
ι	0.001	
κ	0.001	
λ	0.001	
μ	0.001	
ν	0.001	
ξ	0.001	
\omicron	0.001	
π	0.001	
ρ	0.001	
σ	0.001	
τ	0.001	
υ	0.001	
ϕ	0.001	
χ	0.001	
ψ	0.001	
ω	0.001	
Ω	0.001	
Θ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.	

Met 1	Glu	Val	Lys	Leu 5	Glu	Glu	His	Phe	Asn 10	Lys	Thr	Phe	Val	Thr 15	Glu
Asn	Asn	Thr	Ala 20	Ala	Ser	Gln	Asn	Thr 25	Ala	Ser	Pro	Ala	Trp 30	Glu	Asp
Tyr	Arg	Gly 35	Thr	Glu	Asn	Asn	Thr 40	Ser	Ala	Ala	Arg	Asn 45	Thr	Ala	Phe
Pro	Val 50	Trp	Glu	Asp	Tyr	Arg 55	Gly	Ser	Val	Asp	Asp 60	Leu	Gln	Tyr	Phe
Leu 65	Ile	Gly	Leu	Tyr	Thr 70	Phe	Val	Ser	Leu	Leu 75	Gly	Phe	Met	Gly	Asn 80
Leu	Leu	Ile	Leu	Met 85	Ala	Val	Met	Lys	Lys 90	Arg	Asn	Gln	Lys	Thr 95	Thr
Val	Asn	Phe	Leu 100	Ile	Gly	Asn	Leu	Ala 105	Phe	Ser	Asp	Ile	Leu 110	Val	Val
Leu	Phe	Cys 115	Ser	Pro	Phe	Thr	Leu 120	Thr	Ser	Val	Leu	Leu 125	Asp	Gln	Trp
Met 130	Phe	Gly	Lys	Ala	Met	Cys 135	His	Ile	Met	Pro	Phe 140	Leu	Gln	Cys	Val
Ser 145	Val	Leu	Val	Ser	Thr 150	Leu	Ile	Leu	Ile	Ser	Ile 155	Ala	Ile	Val	Arg 160
Tyr	His	Met	Ile 165	Lys	His	Pro	Ile	Ser	Asn 170	Asn	Leu	Thr	Ala	Asn 175	His
Gly	Tyr	Phe	Leu 180	Ile	Ala	Thr	Val	Trp 185	Thr	Leu	Gly	Phe	Ala 190	Ile	Cys
Ser	Pro	Phe 195	Pro	Val	Phe	His	Ser 200	Leu	Val	Glu	Leu	Lys 205	Glu	Thr	Phe
Gly 210	Ser	Ala	Leu	Leu	Ser	Ser 215	Lys	Tyr	Leu	Cys	Val 220	Glu	Ser	Trp	Pro
Ser 225	Asp	Ser	Tyr	Arg	Ile 230	Ala	Phe	Thr	Ile	Ser	Leu 235	Leu	Leu	Val	Gln 240
Tyr	Ile	Leu	Pro 245	Leu	Val	Cys	Leu	Thr	Val 250	Ser	His	Thr	Ser	Val 255	Cys
Arg	Ser	Ile 260	Ser	Cys	Gly	Leu	Ser	His 265	Lys	Glu	Asn	Arg	Leu 270	Glu	Glu
Asn	Glu	Met 275	Ile	Asn	Leu	Thr	Leu 280	His	Pro	Ser	Lys	Lys 285	Ser	Arg	Asp
Gln 290	Ala	Lys	Pro	Pro	Ser	Thr 295	Gln	Lys	Trp	Ser	Tyr 300	Ser	Phe	Ile	Arg

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala
 305 310 315 320
 Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro
 325 330 335
 Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly
 340 345 350
 Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln
 355 360 365
 Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg
 370 375 380
 Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser
 385 390 395 400
 Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn
 405 410 415
 Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu
 420 425 430
 Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu
 435 440 445
 Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp
 450 455 460
 Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met
 465 470 475 480
 His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala
 485 490 495
 Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
 500 505

<210> 23
 <211> 352
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 23
 Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu
 1 5 10 15
 Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
 20 25 30
 Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val

35

40

45

Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu
50 55 60

Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys
65 70 75 80

Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe
85 90 95

Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser
100 105 110

Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met
115 120 125

Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile
130 135 140

Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn
145 150 155 160

Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr
165 170 175

Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val
180 185 190

Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu
195 200 205

Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile
210 215 220

Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val
225 230 235 240

Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met
245 250 255

Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val
260 265 270

Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met
275 280 285

Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile
290 295 300

Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly
305 310 315 320

Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn
325 330 335

Gly Ile Lys Ala Asp Leu Arg Ala Leu Ile His Cys Leu His Met Ser

<210> 24

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 24

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu
1 5 10 15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val
35 40 45

Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu
50 55 60

Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys
65 70 75 80

Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe
85 90 95

Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser
100 105 110

Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met
115 120 125

Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile
130 135 140

Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn
145 150 155 160

Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr
165 170 175

Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val
180 185 190

Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu
195 200 205

Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile
210 215 220

Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val
225 230 235 240

Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser His Lys
245 250 255

Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu Gln Pro
260 265 270

Ser Lys Lys Ser Arg Asn Gln Ala Lys Thr Pro Ser Thr Gln Lys Trp
275 280 285

Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg Tyr Ser Lys Lys Thr
290 295 300

Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser Gln Gly Lys His Leu
305 310 315 320

Ala Val Pro Glu Asn Pro Ala Ser Val Arg Ser Gln Leu Ser Pro Ser
325 330 335

Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe Glu Val Lys Pro Glu
340 345 350

Glu Ser Ser Asp Ala His Glu Met Arg Val Lys Arg Ser Ile Thr Arg
355 360 365

Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
370 375 380

Leu Val Phe Ala Val Ser Trp Met Pro Leu His Val Phe His Val Val
385 390 395 400

Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
405 410 415

Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
420 425 430

Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Gln Arg Asp Leu Gln
435 440 445

Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu
450 455 460

Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu
465 470 475 480

Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn
485 490 495

Glu Lys Ile

<210> 25

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 25

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu
1 5 10 15
Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
20 25 30
Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val
35 40 45
Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu
50 55 60
Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys
65 70 75 80
Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe
85 90 95
Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser
100 105 110
Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met
115 120 125
Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile
130 135 140
Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn
145 150 155 160
Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr
165 170 175
Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val
180 185 190
Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu
195 200 205
Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile
210 215 220
Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val
225 230 235 240
Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met
245 250 255
Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val
260 265 270

Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met
275 280 285

Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile
290 295 300

Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly
305 310 315 320

Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn
325 330 335

Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe
340 345 350

Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His
355 360 365

Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe
370 375 380

Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile
385 390 395

<210> 26

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 26

Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu
1 5 10 15

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp
20 25 30

Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser

115					120					125					
Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys
130						135					140				
His	Pro	Val	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile
145				150						155					160
Ala	Thr	Val	Trp	Thr	Leu	Gly	Leu	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val
				165					170					175	
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Ser	Phe	Gly	Ser	Ala	Trp	Leu
			180					185					190		
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg
		195					200					205			
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu
	210					215					220				
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg
225						230					235				240
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser
				245					250					255	
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Val	Leu	Ile	Leu	Val	Phe
			260					265					270		
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe
			275				280						285		
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile
	290					295					300				
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr
305					310					315					320
Gly	Phe	Leu	Asn	Asn	Gly	Ile	Lys	Ala	Asp	Leu	Met	Ser	Leu	Ile	His
				325					330					335	
Cys	Leu	His	Val	Ser											
			340												

<210> 27

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 27

Met	Gly	Ser	Glu	Ile	Pro	Asp	Tyr	Tyr	Asn	Lys	Thr	Leu	Ala	Ser	Glu
1					5				10					15	

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp
 20 25 30
 Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
 35 40 45
 Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
 50 55 60
 Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
 65 70 75 80
 Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
 85 90 95
 Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
 100 105 110
 Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser
 115 120 125
 Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
 130 135 140
 His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
 145 150 155 160
 Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val
 165 170 175
 Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu
 180 185 190
 Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
 195 200 205
 Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu
 210 215 220
 Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg
 225 230 235 240
 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
 245 250 255
 Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe
 260 265 270
 Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe
 275 280 285
 Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile
 290 295 300
 Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr
 305 310 315 320

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Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn
325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Val Ile Ala Met
340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
355 360 365

Pro Val Ala Leu Lys Lys Ile His Ser Asp Asp Asn Glu Lys Ile
370 375 380

<210> 28
<211> 21
<212> DNA
<213> Homo sapiens

<400> 28
ttttggttgc tgacaaatgt c 21

<210> 29
<211> 26
<212> DNA
<213> Homo sapiens

<400> 29
ccttggtaaa cagtgagaat tattac 26

<210> 30
<211> 455
<212> PRT
<213> Cercopithecus aethiops

<400> 30
Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp
1 5 10 15

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Val	Met	Cys	His	Ile	Met	Pro
		115					120					125			
Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile	Ser
	130					135					140				
Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn	Asn
145					150					155					160
Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr	Leu
				165					170					175	
Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val	Glu
			180					185					190		
Leu	Gln	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Arg	Tyr	Leu	Cys
		195					200					205			
Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser
	210					215					220				
Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser
225					230					235					240
His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	Asn	Lys	Glu
				245					250					255	
Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	His	Pro	Ser
			260					265					270		
Arg	Lys	Ile	Gly	Pro	Gln	Val	Lys	Leu	Ser	Gly	Ser	His	Lys	Trp	Ser
		275					280					285			
Tyr	Ser	Phe	Ile	Lys	Lys	His	Arg	Arg	Arg	Tyr	Ser	Lys	Lys	Thr	Ala
	290					295					300				
Cys	Val	Leu	Pro	Ala	Pro	Glu	Arg	Pro	Ser	Gln	Glu	Asn	His	Ser	Arg
305					310					315					320
Ile	Leu	Pro	Glu	Asn	Phe	Gly	Ser	Val	Arg	Ser	Gln	Leu	Ser	Ser	Ser
				325					330					335	
Ser	Lys	Phe	Ile	Pro	Gly	Val	Pro	Thr	Cys	Phe	Glu	Ile	Lys	Pro	Glu
			340					345					350		
Glu	Asn	Ser	Asp	Val	His	Glu	Leu	Arg	Val	Lys	Arg	Ser	Val	Thr	Arg
		355					360					365			
Ile	Lys	Lys	Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile
	370					375					380				
Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val
385					390					395					400
Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val
				405					410					415	

